Type: Poster Presentation

Final Abstract Number: 52.005
Session: Epidemiology and Public Health II
Date: Friday, April 4, 2014
Time: 12:45-14:15
Room: Ballroom

Common infectious and communicable diseases among a nomadic Fulani population in Kano, Nigeria

Z.G. Habib[1], M.M. Dalhat[2], H. Muhammad[3,*], M.M. Bello[4], A.U. Bello[5], A.M. Yakasai[6], A.H. Sadauki[7], U.-F. Abdullahi[7], B.A. Gwaram[4], F. Sarkin-Fada[8], K.M. Karaye[8], I. Abdulkadir[5], A.G. Habib[8]

[1] *University of Abuja Teaching Hospital, Gwagwalada, Abuja, Gwagwalada, Nigeria*
[2] *Aminu Kano Teaching Hospital, Kano, Kano, Nigeria*
[3] *Bayero University, Kano, Nigeria*
[4] *Bayero University, Kano, Kano, Nigeria*
[5] *Ahmadu Bello Univesity, Zaria, Nigeria*
[6] *Murtala Muhammad Specialist Hospital, Kano, Nigeria*
[7] *Aminu Kano Teaching Hospital, Kano, Nigeria*
[8] *Bayero University Kano, Kano, Nigeria*

Background: Infectious diseases are an important cause of morbidity and mortality in sub-Saharan Africa. Access to healthcare among nomads has been identified as a major deterrent against effective control, elimination and eradication of infectious diseases in Nigeria. We conducted a community survey among nomadic Fulanis in Kano state to determine the prevalence of common infectious diseases.

Methods & Materials: We interviewed consenting adults 15 years and above to obtain socio-demographic information, social habits and symptoms of common infectious diseases. Rapid Diagnostic Tests (RDT) and tuberculin sensitivity test (TST) were conducted to determine prevalence of malaria antigenaemia and exposure to Mycobacterium. Focussed group discussions were conducted with selected members of the community to determine their felt needs, knowledge, perceptions and awareness about preventive measures against common infectious diseases with emphasis on malaria, tuberculosis, sexually transmitted infections (STI), and human immunodeficiency virus infection (HIV).

Results: Of 229 respondent interviewed, 100 (43.7%) were females. A total of 153 (66.8%) respondents had fever within the previous 3 months. Cough and urethral discharge were documented among 29 (14.1%) and 31 (13.9%) respectively. Malaria RDT positivity was found among 24(10.5%) subjects. Of the 167 respondents who consented and had TST read, 45 (26.9%) were positive. Sixty five (34.0%) respondents reported having sick animals; 51 (78.5%) of which had cough. Findings from FGDs conducted revealed that majority of the respondents consider malaria as a common cause of morbidity and mortality especially among paediatric age groups. They also consider tuberculosis as common with potential for animal to human transmission. However, they failed to link seeking treatment and care for their sick animals as a preventive measure against common human infectious diseases. Regarding appropriate preventive measures against malaria and other infectious diseases, the respondents failed to demonstrate adequate knowledge. Majority of the respondents identified as their priority needs potable water supply, access roads and health facility in order of priority.

Conclusion: Communicable diseases are common among nomadic Fulanis and their livestock. Lack of access to health care facilities for this vulnerable and neglected population could militate against effective control of infectious diseases. Diseases control programmes should evolve innovative ways of reaching nomads with their interventions.

http://dx.doi.org/10.1016/j.ijid.2014.03.922

Type: Poster Presentation

Final Abstract Number: 52.006
Session: Epidemiology and Public Health II
Date: Friday, April 4, 2014
Time: 12:45-14:15
Room: Ballroom

Molecular epidemiology of Vibrio choleraeO1 in Mozambique

J.P. Langa[1,*], E. Taviani[2], C. Sema[1], N. De Deus[1], M.M. Colombo[3]

[1] *Instituto Nacional de Saúde, Mozambique, Maputo, Mozambique*
[2] *Centro de Biotecnologia, Universidade E. Mondlane, Maputo, Mozambique*
[3] *Universita di Roma, Rome, Italy*

Background: Africa is increasingly affected by cholera,accounting in 2009for 98% of the officially reported cases worldwide. In Mozambique cholera appeared in early 1970's when the seventh pandemic entered Africa from the Indian Subcontinent. In the following decades, several epidemics were registered in the country, with the '97-'99 being the most extended. Since then, Mozambique is considered an endemic area for cholera, characterized by outbreaks occurring yearly with a seasonal pattern. Despite improving sanitary conditions, cholera continues to represent a major public health issue for the country:12.819 cases were reported in 2012, with a 1,1% mortality rate. From an epidemiological standpoint, the cholera seventh pandemic is caused by V. cholerae O1 strains genetically related but differentiated by their content of mobile genetic elements (the mobilome), such asphages, Pathogenicity Islands and Integrative Conjugative Elements. At least five pandemic variants are thought to have originated in the Indian Subcontinent and spread worldwide at different times.

Methods & Materials: In this study we investigated the epidemiology of cholera in Mozambique through the molecular characterization of clinical *V. cholerae* O1 isolated during 1997-1999 and 2012-2013 epidemics. By detecting and characterizing seven genetic elements, we obtained the *mobilome* profile of each isolate and, by comparing it to known seventh pandemic reference strains, it was possible to discern among different *V. cholerae* O1 variants present in the country.

Results: According to our results, during 1997-99, the epidemic strains showed two genetic profiles, both related to the pandemic clone originated from India and reported in other African countries in those years. Differently, isolates from 2012-2013 outbreaks showed a genetic background related to the more recent pandemic clone, at first reported in India and currently the prevalent causative agent of cholera worldwide.

Conclusion: Therefore, our study highlighted the possibility that, despite cholera is endemic in Mozambique, the epidemiology of the disease in the past 20 years has been strongly influenced by the cholera seventh pandemic waves originated in the Indian

Subcontinent. Our results not only add new insights on the evolutionary history of cholera, but also provide valuable information to modulate the public health response to the disease.

http://dx.doi.org/10.1016/j.ijid.2014.03.923

Type: Poster Presentation

Final Abstract Number: 52.007
Session: Epidemiology and Public Health II
Date: Friday, April 4, 2014
Time: 12:45-14:15
Room: Ballroom

Misdiagnosed outbreak of bartonella bacilliformis in Peruvian Amazon department

A. Cornejo[1], V. Casabona[2], C.S.P. Gomes[3,*], C. Tinco[4], S. Martinez-Puchol[5], L. Suarez[6], J. Ruiz[7], J. del Valle[8]

[1] *Universidad Peruana de Ciencias Aplicadas (UPC) e Instituto de Investigaciòn Nutricional (IIN), Lima, PE, Peru*
[2] *Universidad Peruana de Ciencias Aplicadas. Instituto de Investigación Nutricional, Lima, Peru*
[3] *Barcelona Centre for International Health Research, Barcelona, Spain*
[4] *Instituto de Investigación Nutricional, Lima, Peru*
[5] *Barcelona Centre for International Health Research, Barcelona, Spain*
[6] *Facultad de Ciencias de la Salud, Universidad Peruana de Ciencias Aplicadas, Lima, Peru*
[7] *Centre de Recerca en Salut Internacional de Barcelona, Hospital Clinic/Institut d'Investigacions Biomèdiques August Pi i Sunyer, Barcelona, Spain*
[8] *Instituto de Investigación Nutricional (IIN) y UPC-Perú, PERU, PE, Peru*

Background: In March 2013, the presence of an outbreak of *Bartonella bacilliformis* in the Rodriguez de Mendoza (Amazonas department, Peru) was reported. *B. bacilliformis* is an endemic pathogen of the Andean region, responsible for Carrion's disease. One of the main problems of this illness is the lack of adequate technical and human resources for proper diagnosis in endemic rural areas. The objective of this study was to characterize a supposed *B. bacilliformis* outbreak, internationally informed in Rodriguez de Mendoza province.

Methods & Materials: Fifty-three blood samples were recovered from people diagnosed with Carrion's disease, either by optical microscopy and/or clinical manifestations. In all cases epidemiological and clinical data were recorded. The samples were cultured on Columbia Agar adding 10% of sheep blood and incubated at 28 °C for a period of 10 weeks. Every 14 days the plates were visually inspected to detect any bacterial growth. Additionally, the DNA was directly extracted from blood and 2 different *16S rRNA* PCR schemes were used, one specific for *Bartonella* genus and other using universal primers. Twenty-six amplified products of universal *16S rRNA* were randomly recovered and sequenced.

Results: The main clinical presentations reported were headache (51%), physical discomfort (51%), chill (32%) and fever (24, 5%). Only 3 blood cultures were positive. No positive PCR was obtained when using the *Bartonella* specific PCR either on blood or on cultured bacteria. However, all the PCR with the universal primers were positive. The sequenced 26 (49%) samples were identified as *Sphingomonas* spp. being this microorganism the causative agent of this outbreak. In 17% of the cases, patients were reported to have aquatic activities.

Conclusion: Several *Sphingomonas* spp. infections in humans have been reported, mostly limited to sporadic case reports or intra-hospitalary outbreaks, but as far as we know this is the first outbreak of *Sphingomonas* spp. described in a non-hospital environment. The association between 17% of patients with aquatic activities suggests that this was the most feasible transmission way.

Training of health staff and development of new diagnostic able to be implemented in rural endemic areas is urgent in order to overcome wrong diagnostics and avoid wrong treatments.

http://dx.doi.org/10.1016/j.ijid.2014.03.924

Type: Poster Presentation

Final Abstract Number: 52.008
Session: Epidemiology and Public Health II
Date: Friday, April 4, 2014
Time: 12:45-14:15
Room: Ballroom

Malaria among sickle cell anaemia (SCA) patients in a nomadic population

M.M. Dalhat[1,*], B.A. Gwaram[2], H. Muhammad[3], Z.G. Habib[4], M.M. Bello[5], A.M. Yakasai[6], A.H. Sadauki[7], H. Aliyu[7], Z.G. Vandi[7], F. Sarkin-Fada[5], K.M. Karaye[8], A.G. Habib[8]

[1] *Aminu Kano Teaching Hospital, Kano, Kano, Kano, Nigeria*
[2] *Bayero University, Kano, Kano, Kano, Nigeria*
[3] *Bayero University Kano, Kano, Kano, Nigeria*
[4] *University of Abuja Teaching Hospital, Gwagwalada, Abuja, Gwagwalada, Abuja, Nigeria*
[5] *Bayero University, Kano, Kano, Nigeria*
[6] *Murtala Muhammed Specialist Hospital, Kano, Nigeria*
[7] *Aminu Kano Teaching Hospital, Kano, Kano, Nigeria*
[8] *Bayero University Kano, Kano, Nigeria*

Background: Nigeria has one of the world's highest burdens of malaria in the world. Nomadic Fulanis in northern-Nigeria have been identified as a vulnerable group, often neglected during planning and implementation of health interventions. Nomadic lifestyle, common practice of consanguineous marriages and poor access to preventive and curative strategies against malaria make sickle cell anaemia common and expose them to devastating effects of malaria. We conducted a cross-sectional study in a nomadic Fulani setting in Kano state, Nigeria to determine burden and effects of malaria in the community.

Methods & Materials: We administered structured questionnaires to individuals 15 years and above to obtain sociodemographic information, consanguinity and symptoms of malaria. We conducted on-the-spot malaria rapid diagnostic test (RDT) and collected blood sample for haematocrit and haemoglobin electrophoresis. We also conducted Focussed Group Discussions (FGD) with selected members of the community to determine knowledge, attitude and preventive practices against malaria and SCA. We compared prevalence of malaria, consanguinity and haemoglobin genotypes within the community.

Results: A total 229 subjects were interviewed, among which100 (43.7%) were females. Median age (range) was 35 yrs (15 – 80 yrs). More than two-thirds of the women 72 (72.0%) were of reproductive age. Symptoms of malaria and positive RDT